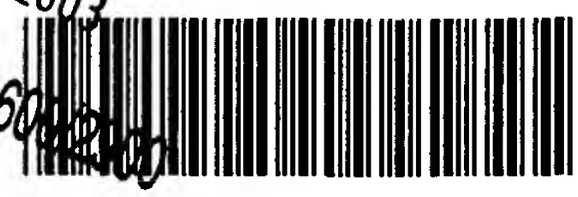

RAW SEQUENCE LISTING DATE: 03/20/2003
PATENT APPLICATION: **US/09/835,107A** TIME: 16:05:40

Input Set : **A:\seqlist.txt**
Output Set: **N:\CRF4\03202003\I835107A.raw**

```
 3 <110> APPLICANT: University of British Columbia, et al.
 5 <120> TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
 7 <130> FILE REFERENCE: 80021-255
 9 <140> CURRENT APPLICATION NUMBER: US 09/835,107A
10 <141> CURRENT FILING DATE: 2001-04-12
12 <150> PRIOR APPLICATION NUMBER: CA 2,305,036
13 <151> PRIOR FILING DATE: 2000-04-12
15 <150> PRIOR APPLICATION NUMBER: US 60/232,425
16 <151> PRIOR FILING DATE: 2000-09-14
18 <150> PRIOR APPLICATION NUMBER: CA 2,335,109
19 <151> PRIOR FILING DATE: 2001-02-23
21 <160> NUMBER OF SEQ ID NOS: 31
23 <170> SOFTWARE: PatentIn Ver. 2.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 67
27 <212> TYPE: PRT
28 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <223> OTHER INFORMATION: SDF-1 alpha
33 <220> FEATURE:
34 <221> NAME/KEY: MISC_FEATURE
35 <222> LOCATION: (1)..(67)
36 <223> OTHER INFORMATION: A pegylation moiety may be provided at any position on the
37       sequence.
39 <400> SEQUENCE: 1
40 Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser
41   1               5                  10                  15
43 His Val Ala Arg Ala Asn Val Lys His Leu Lys Ile Leu Asn Thr Pro
44              20                  25                  30
46 Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn Asn Arg Gln
47          35                  40                  45
49 Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys
50      50                  55                  60
52 Ala Leu Asn
53  65
56 <210> SEQ ID NO: 2
57 <211> LENGTH: 93
58 <212> TYPE: PRT
59 <213> ORGANISM: Homo sapiens
61 <220> FEATURE:
62 <223> OTHER INFORMATION: SDF-1 Precursor, PBSF
64 <220> FEATURE:
65 <221> NAME/KEY: MISC_FEATURE
```

RAW SEQUENCE LISTING DATE: 03/20/2003
PATENT APPLICATION: **US/09/835,107A** TIME: 16:05:40

Input Set : **A:\seqlist.txt**
Output Set: **N:\CRF4\03202003\I835107A.raw**

<222> LOCATION: (1)..(93)
<223> OTHER INFORMATION: A pegylation moiety may be provided at any position on the sequence.

<400> SEQUENCE: 2

```
Met Asn Ala Lys Val Val Val Val Leu Val Leu Val Leu Thr Ala Leu
 1               5                  10                  15
Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys
            20                  25                  30
Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys
        35                  40                  45
Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys
    50                  55                  60
Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln
65                  70                  75                  80
Glu Tyr Leu Glu Lys Ala Leu Asn Lys Arg Phe Lys Met
                85                  90
```

<210> SEQ ID NO: 3
<211> LENGTH: 93
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<223> OTHER INFORMATION: SDF-1 beta
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(93)
<223> OTHER INFORMATION: A pegylation moiety may be provided at any position on the sequence.

<400> SEQUENCE: 3

```
Met Asn Ala Lys Val Val Val Val Leu Val Leu Val Leu Thr Ala Leu
 1               5                  10                  15
Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys
            20                  25                  30
Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys
        35                  40                  45
Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys
    50                  55                  60
Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln
65                  70                  75                  80
Glu Tyr Leu Glu Lys Ala Leu Asn Lys Arg Phe Lys Met
                85                  90
```

<210> SEQ ID NO: 4
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthesised in Laboratory: SDF-1(1-17): or CTCE9902

<400> SEQUENCE: 4

```
Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser
```

RAW SEQUENCE LISTING DATE: 03/20/2003
PATENT APPLICATION: **US/09/835,107A** TIME: 16:05:40

Input Set : **A:\seqlist.txt**
Output Set: **N:\CRF4\03202003\I835107A.raw**

```
135   1               5                  10                  15
137 His
141 <210> SEQ ID NO: 5
142 <211> LENGTH: 6
143 <212> TYPE: PRT
144 <213> ORGANISM: Artificial Sequence
146 <220> FEATURE:
147 <223> OTHER INFORMATION: Synthesised in Laboratory
149 <400> SEQUENCE: 5
150 Arg Phe Phe Glu Ser His
151   1               5
154 <210> SEQ ID NO: 6
155 <211> LENGTH: 9
156 <212> TYPE: PRT
157 <213> ORGANISM: Artificial Sequence
159 <220> FEATURE:
160 <223> OTHER INFORMATION: Synthesised in Laboratory
162 <400> SEQUENCE: 6
163 Lys Pro Val Ser Leu Ser Tyr Arg Cys
164   1               5
167 <210> SEQ ID NO: 7
168 <211> LENGTH: 9
169 <212> TYPE: PRT
170 <213> ORGANISM: Artificial Sequence
172 <220> FEATURE:
173 <221> NAME/KEY: DISULFID
174 <222> LOCATION: (9)
175 <223> OTHER INFORMATION: Disulphide linkage may form between two cys
176       residues at position 9 of each of two monomers
177       thereby forming a dimer.
179 <220> FEATURE:
180 <223> OTHER INFORMATION: Synthesised in Laboratory:
181       SDF-1(1-9)2-C9/C9-cysteine dimer: or CTCE9901
183 <400> SEQUENCE: 7
184 Lys Pro Val Ser Leu Ser Tyr Arg Cys
185   1               5
188 <210> SEQ ID NO: 8
189 <211> LENGTH: 9
190 <212> TYPE: PRT
191 <213> ORGANISM: Artificial Sequence
193 <220> FEATURE:
194 <223> OTHER INFORMATION: Synthesised in Laboratory
196 <220> FEATURE:
197 <221> NAME/KEY: BINDING
198 <222> LOCATION: (9)
199 <223> OTHER INFORMATION: Linking Moiety (may be lysine with both the alpha and the
200       epsilon amino groups of the lysine being associated with
201       the covalent (amide) bond formation) may bind here allowing
202       formation of a dimer.
```

RAW SEQUENCE LISTING DATE: 03/20/2003
PATENT APPLICATION: **US/09/835,107A** TIME: 16:05:40

Input Set : **A:\seqlist.txt**
Output Set: **N:\CRF4\03202003\I835107A.raw**

```
204 <400> SEQUENCE: 8
205 Lys Pro Val Ser Leu Ser Tyr Arg Cys
206   1               5
209 <210> SEQ ID NO: 9
210 <211> LENGTH: 8
211 <212> TYPE: PRT
212 <213> ORGANISM: Artificial Sequence
214 <220> FEATURE:
215 <223> OTHER INFORMATION: Synthesised in Laboratory
217 <220> FEATURE:
218 <221> NAME/KEY: BINDING
219 <222> LOCATION: (8)
220 <223> OTHER INFORMATION: Linking Moiety (may be lysine with both the alpha and the
221       epsilon amino groups of the lysine being associated with
222       the covalent (amide) bond formation) may bind here allowing
223       formation of a dimer.
225 <400> SEQUENCE: 9
226 Lys Pro Val Ser Leu Ser Tyr Arg
227   1               5
230 <210> SEQ ID NO: 10
231 <211> LENGTH: 30
232 <212> TYPE: PRT
233 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
236 <221> NAME/KEY: DOMAIN
237 <222> LOCATION: (15)..(17)
238 <223> OTHER INFORMATION: spacer monomers (such as the illustrated glycine
239       G's) may be used in variable numbers, such as 2, 3
240       or 4 glycines.
242 <220> FEATURE:
243 <223> OTHER INFORMATION: Synthesised in Laboratory:
244       SDF-1(1-14)-(G)3-SDF-1(55-67) acid
246 <400> SEQUENCE: 10
247 Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly
248   1               5                  10                  15
250 Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn
251               20                  25                  30
254 <210> SEQ ID NO: 11
255 <211> LENGTH: 31
256 <212> TYPE: PRT
257 <213> ORGANISM: Artificial Sequence
259 <220> FEATURE:
260 <221> NAME/KEY: DOMAIN
261 <222> LOCATION: (16)..(19)
262 <223> OTHER INFORMATION: spacer monomers (such as the illustrated glycine
263       G's) may be used in variable numbers, such as 2, 3
264       or 4 glycines.
266 <220> FEATURE:
267 <223> OTHER INFORMATION: Synthesised in Laboratory:
```

RAW SEQUENCE LISTING DATE: 03/20/2003
PATENT APPLICATION: **US/09/835,107A** TIME: 16:05:40

Input Set : **A:\seqlist.txt**
Output Set: **N:\CRF4\03202003\I835107A.raw**

SDF-1(1-14)-(G)4-SDF-1(55-67) acid: or CTCE0013

<400> SEQUENCE: 11

Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly
1 5 10 15

Gly Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn
20 25 30

<210> SEQ ID NO: 12
<211> LENGTH: 30
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (15)..(17)
<223> OTHER INFORMATION: spacer monomers (such as the illustrated glycine G's) may be used in variable numbers, such as 2, 3 or 4 glycines.
<220> FEATURE:
<223> OTHER INFORMATION: Synthesised in Laboratory: SDF-1(1-14)-(G)3-SDF-1(55-67) amide
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (30)
<223> OTHER INFORMATION: AMIDATION

<400> SEQUENCE: 12

Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly
1 5 10 15

Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn
20 25 30

<210> SEQ ID NO: 13
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<221> NAME/KEY: DOMAIN
<222> LOCATION: (15)..(18)
<223> OTHER INFORMATION: spacer monomers (such as the illustrated glycine G's) may be used in variable numbers, such as 2, 3 or 4 glycines.
<220> FEATURE:
<223> OTHER INFORMATION: Synthesised in Laboratory: SDF-1(1-14)-(G)4-SDF-1(55-67) amide: or CTCE0017
<220> FEATURE:
<221> NAME/KEY: MOD_RES
<222> LOCATION: (31)
<223> OTHER INFORMATION: AMIDATION

<400> SEQUENCE: 13

Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly
1 5 10 15

Gly Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/835,107A**

DATE: 03/20/2003
TIME: 16:05:41

Input Set : **A:\seqlist.txt**
Output Set: **N:\CRF4\03202003\I835107A.raw**